

MAY 19 2009

Application No.: 10/533,459

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Docket No.: 63139(47992)

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

Listing of The Claims:

1. – 19. (Cancelled)

20. (Currently Amended) A microarray of genes, or polynucleotide fragments or RNA transcripts thereof for distinguishing a neuroendocrine tumor cell, said microarray comprising a solid support having greater than 10 genes, or polynucleotide fragments or RNA transcripts thereof, distinguishably arrayed in spaced apart regions, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) cell, a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell, a typical carcinoid (TC) neuroendocrine tumor cell, or an atypical carcinoid (AC) neuroendocrine tumor cell, relative to a normal cell or a cell belonging to a different neuroendocrine tumor cell type, to permit said microarray to distinguish a neuroendocrine tumor cell, and wherein said genes or polynucleotide fragments or RNA transcripts thereof includes GGH, or a polynucleotide fragment or RNA transcript thereof.

21. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a neuroendocrine tumor cell relative to a normal cell to permit said microarray to distinguish between a neuroendocrine tumor cell and a normal cell.

22. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC)

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neuroendocrine tumor cell and a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell.

23. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to a typical carcinoid (TC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and a typical carcinoid (TC) neuroendocrine tumor cell.

24. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a small cell lung cancer (SCLC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a small cell lung cancer (SCLC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

25. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell relative to a typical carcinoid (TC) neuroendocrine tumor cell to permit said microarray to distinguish between a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell and a typical carcinoid (TC) neuroendocrine tumor cell.

26. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a large cell neuroendocrine carcinoma (LCNEC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a large cell neuroendocrine carcinoma

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(LCNEC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

27. (Original) The microarray of claim 20, wherein said microarray comprises a sufficient number of genes, or polynucleotide fragments or RNA transcripts thereof, that are differentially expressed in a typical carcinoid (TC) neuroendocrine tumor cell relative to an atypical carcinoid (AC) neuroendocrine tumor cell to permit said microarray to distinguish between a typical carcinoid (TC) neuroendocrine tumor cell and an atypical carcinoid (AC) neuroendocrine tumor cell.

28. (Original) The microarray of claim 20, wherein said genes or polynucleotide fragments or RNA transcripts thereof of said microarray include one or more genes selected from the group consisting of C5, CPE, GRIA2, RIMS2, ORC4L, CSF2RB, GGH, NPAT, NR3C1, P311, PRKAA2, PTK6, APRT, ARF4L, ARHGD1A, ARL7, ATP6F, CDC20, CDC34, CLDN11, COMT, CSTF1, DDX28, DHCR7, ERP70, FEN1, GCN1L1, GNB1, GUK1, HDAC7A, ITPA, JUP, KIAA0469, KRT5, PDAP1, PGAM1, PHB, POLA2, POLD2, POLE3, PYCRI, SIP2-28, SIVA, SURF 1, TADA3L, TK1, TYMSTR, and VATI, or a polynucleotide fragment or RNA transcript thereof.

29. (Currently Amended The ~~method~~microarray of claim 23, wherein said genes or polynucleotide fragments or RNA transcripts thereof of said microarray include one or more genes selected from the group consisting of GGH and CPE, or a polynucleotide fragment or RNA transcript thereof.

30 (Cancelled)

31. (Cancelled)

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